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OM protein - protein search, using sw model

Run on: October 22, 2004, 13:36:34 ; Search time 158 seconds
(without alignments)
95.358 Million cell updates/sec

Title: US-09-763-982B-1
Perfect score: 243
Sequence: 1 NQSNFGFMKGNGFRSSG.....GGGQYFAKPRNQGGGGC 42

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	243	100.0	42	3	AAV82221	Modified
2	228	93.8	76	5	ABP42473	Human ova
3	228	93.8	250	4	ABG03369	Novel hum
4	228	93.8	296	4	ABG09555	Novel hum
5	228	93.8	296	4	ABG04261	Novel hum
6	228	93.8	296	4	ABG03366	Novel hum
7	228	93.8	296	4	ABG15176	Novel hum
8	228	93.8	296	4	AU29983	Novel hum
9	228	93.8	298	7	ADJ69744	Human hea
10	228	93.8	319	7	ADJ69744	Rat Prote
11	228	93.8	320	2	AAW55828	Human het
12	228	93.8	320	4	AAW55828	Human het
13	228	93.8	320	4	AAW55828	Human het
14	228	93.8	320	4	ABG00955	Novel hum
15	228	93.8	320	5	ABG00955	Novel hum
16	228	93.8	320	8	ADJ17083	Human hnr
17	228	93.8	351	7	ADJ60577	Human con
18	228	93.8	369	4	ABG15179	Novel hum
19	228	93.8	372	6	ABG052967	Human spl
20	228	93.8	470	4	ABG04264	Novel hum
21	228	93.8	474	4	ABG04458	Novel hum
22	228	93.8	1205	4	ABG15312	Novel hum
23	228	93.8	1205	4	ABG05068	Novel hum
24	225	92.6	95	4	ABG15177	Novel hum
25	225	92.6	95	4	ABG27119	Novel hum

26	225	92.6	95	4	ABG09556	Novel hum
27	225	92.6	312	4	ABG06528	Novel hum
28	225	92.6	320	7	ADJ57410	Human Pro
29	222	91.4	1214	4	ABG27121	Novel hum
30	218	89.7	324	6	ABU11521	Human MDD
31	216	88.9	38	2	AAV67200	Novel hum
32	216	88.9	38	3	AAV82223	M9 nuclea
33	216	88.9	38	4	AAE02957	Human RNP
34	216	88.9	44	2	AAW08405	M9 includ
35	212.5	87.4	41	6	ABP56848	Peptide M
36	197	81.1	254	4	ABG16296	Novel hum
37	197	81.1	254	4	ABG04260	Novel hum
38	197	81.1	254	4	ABG04455	Novel hum
39	197	81.1	237	4	ABG00954	Novel hum
40	193	79.4	558	4	ABG15178	Novel hum
41	193	79.4	558	4	ABG09557	Novel hum
42	193	79.4	558	4	ABG04262	Novel hum
43	184	75.7	369	4	ABG04454	Novel hum
44	184	75.7	370	4	ABG05066	Novel hum
45	179	73.7	133	4	ABG03368	Novel hum

ALIGNMENTS

RESULT 1
AAV82221
ID AAV82221 standard; peptide; 42 AA.
XX AAV82221;
XX
XX 13-JUN-2000 (first entry)
XX
XX Modified M9 nuclear targeting peptide SEQ ID NO:1.
XX Human; M9; heteronuclear ribonuclear protein type 1; hnRNP A1; NTP;
XX nuclear targeting peptide; peptide scaffold; gene transfer; NLS;
XX nuclear localisation signal; antiarteriosclerotic; vasotropic;
XX Gene therapy; atherosclerosis; restenosis; angioplasty.
XX Homo sapiens.
XX WO200012114-A1.
XX
XX 09-MAR-2000.
XX
XX 01-SEP-1999; 99WO-US020122.
XX
XX 01-SEP-1998; 98US-0098791P.
XX (UYPE-) UNIV PENNSYLVANIA.
XX Diamond SL;
XX WPI; 2000-256490/22.
XX Delivering molecules to nuclei of eukaryotic cells for use in gene transfer methods uses a nuclear targeting peptide which contains a non-classical nuclear localization signal.
XX Claim 8; Page 17; 40pp; English.
XX
XX The present invention describes a composition for enhancing delivery of a molecule to the nucleus of eukaryotic cells, comprising a nuclear targeting peptide (NTP) containing a non-classical nuclear localisation signal (NLS). The composition can have antiarteriosclerotic and vasotropic activities, and can be used in gene therapy. The composition is used to treat a patient having a condition associated with lack of expression of a selected nucleic acid sequence. The compositions are particularly useful for arterial gene transfer, to treat atherosclerosis and restenosis following angioplasty. The present sequence represents a specifically claimed NTP which comprises the human heteronuclear ribonuclear protein type 1 (hnRNP A1) M9 epitope with a carboxy terminal

CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 250 AA;

Query Match 93.8%; Score 228; DB 4; Length 250;
 Best Local Similarity 100.0%; Pred. No. 2.1e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGGYGG 40
 DB 198 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGGYGG 237

RESULT 4
 ABG09555
 ID ABG09555 standard; protein; 296 AA.

XX AC ABG09555;
 DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #9546.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
 XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS73742.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 39914; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders

CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 296 AA;

Query Match 93.8%; Score 228; DB 4; Length 296;
 Best Local Similarity 100.0%; Pred. No. 2.5e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGGYGG 40
 DB 244 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGGYGG 283

RESULT 5
 ABG04261
 ID ABG04261 standard; protein; 296 AA.

XX AC ABG04261;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #4252.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.
 XX WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS68448.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 34620; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 296 AA;

Query Match 93.8%; Score 228; DB 4; Length 296;
 Best Local Similarity 100.0%; Pred. NO. 2.5e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
 |||||
 Db 244 NQSNFPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 283

RESULT 6
 ABG03366
 ID ABG03366 standard; protein; 296 AA.

AC ABG03366;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #337.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS67553.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

PS Claim 20; SEQ ID NO 33725; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 296 AA;

Query Match 93.8%; Score 228; DB 4; Length 296;
 Best Local Similarity 100.0%; Pred. NO. 2.5e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
 |||||
 Db 244 NQSNFPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 283

RESULT 7
 ABG15176
 ID ABG15176 standard; protein; 296 AA.

AC ABG15176;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #15167.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI; 2001-639362/73.

DR N-PSDB; AAS79363.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

PS Claim 20; SEQ ID NO 45535; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic

CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 296 AA;

Query Match 93.8%; Score 228; DB 4; Length 296;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGYYG 40
|||
Db 244 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGYYG 283
|||

RESULT 8
AAU29983
ID AAU29983 standard; protein; 296 AA.
AC AAU29983;
DT 18-DEC-2001 (first entry)
DE Novel human secreted protein #474.
XX Human; vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.
XX
OS Homo sapiens.
XX
FN WO200179449-A2.
PD 25-OCT-2001.
PF 16-APR-2001; 2001WO-US008656.
PR 18-APR-2000; 2000US-0052929.
PR 26-JAN-2001; 2001US-00770160.
XX (HYSE-) HYSEQ INC.
XX Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-611725/70.
DR
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy.
XX
PS Claim 20; Page 217; 765pp; English.

XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising the
CC nucleic acids encoding the polypeptides and cells genetically engineered
CC to express them are also useful for producing the proteins. The proteins
CC are useful in genetic vaccination, testing and therapy, and can be used
CC as nutritional supplements. They may be used to increase stem cell
CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon
CC and/or nerve tissue growth or regeneration; immune suppression and/or
CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.
CC AAU29510-AAU33304 represent the amino acid sequences of novel human
XX secreted proteins of the invention

SQ Sequence 296 AA;
Query Match 93.8%; Score 228; DB 4; Length 296;

Best Local Similarity 100.0%; Pred. No. 2.5e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGYYG 40
|||
Db 244 NOSSNFGPMKGNFGRRSGPYGGGQYFAKPRNQGYYG 283
|||

RESULT 9
ADJ69744
ID ADJ69744 standard; protein; 298 AA.
AC ADJ69744;
DT 06-MAY-2004 (first entry)
DE Human heat mitochondrial protein as a therapeutic target SeqID1550.

XX Mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis; LHON;
KW Leber's hereditary optic neuropathy; lactic acidosis and stroke; MELAS;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.

XX Homo sapiens.
OS
XX WO2003087768-A2.
FN
XX 23-OCT-2003.
PD
XX 04-APR-2003; 2003WO-US010870.
PF
XX 12-APR-2002; 2002US-0372843P.
PR
XX 17-JUN-2002; 2002US-0389987P.
PR
XX 20-SEP-2002; 2002US-0412418P.
PR

XX (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.

XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
XX Warnock DE;
XX WPI; 2003-845369/78.

XX Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function.
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

XX Claim 1; SEQ ID NO 1550; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nontropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 298 AA;
Query Match 93.8%; Score 228; DB 7; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.5e-18;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
Best Local Similarity 100.0%; Pred. No. 2.7e-18; Length 319;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 246 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 285

RESULT 10
AADE57408
ID ADE57408 standard; protein; 319 AA.
XX AC ADE57408;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein P04256, SEQ ID NO 3269.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX XX (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
XX DR GENBANK; P04256.
XX XX
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017pp; English.
XX XX
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 319 AA;
Query Match 93.8%; Score 228; DB 7; Length 319;
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
Db 267 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 306

RESULT 11
AAW55828
ID AAW55828 standard; protein; 320 AA.
XX AC AAW55828;
XX DT 20-JUL-1998 (first entry)
XX DE Human heterogeneous nuclear ribonucleoprotein core protein A1.
XX KW Human; heterogeneous nuclear ribonucleoprotein; core protein; hnRNP;
XX KW RNA binding protein; detection; coding region.
XX OS Homo sapiens.
XX PN JP10023893-A.
XX PD 27-JAN-1998.
XX PF 09-JUL-1996; 96JP-00179521.
XX PR 09-JUL-1996; 96JP-00179521.
XX PA (HITA) HITACHI LTD.
XX DR WPI; 1998-152795/14.
XX DR N-PSDB; AAV25978.
XX XX
XX PT Detection of protein code region on DNA base sequence - using method
XX PT which reduces interference from noncoding region.
XX PS Disclosure; Fig 2-5; 16pp; Japanese.
XX XX
XX CC The present sequence represents the human heterogeneous nuclear
XX CC ribonucleoprotein (hnRNP) core protein A1, which is used to exemplify the
XX CC method of the present invention. The hnRNP A1 gene can be found on the
XX CC genbank database accession number X12671, NID G32344. The present
XX CC invention describes a method for the detection of a protein coding region
XX CC in a DNA base sequence by judging the probability where a specific
XX CC sequence will be found. The method comprises utilizing the appearance
XX CC frequency in the coding and the noncoding regions. The method allows
XX CC noise in the noncoding region to be reduced

SQ Sequence 320 AA;
Query Match 93.8%; Score 228; DB 2; Length 320;
Best Local Similarity 100.0%; Pred. No. 2.7e-18;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
Db 268 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 307

RESULT 12
AAB48966
ID AAB48966 standard; protein; 320 AA.
XX AC AAB48966;
XX DT 27-MAR-2001 (first entry)
XX XX

DE Human heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1).
 XX
 KW Human hnRNP A1; heterogeneous nuclear ribonucleoprotein A1;
 KW heterogeneous nuclear ribonucleoprotein core protein A1; p40CRS;
 KW mRNA processing; transport; stabilisation; alternative splicing;
 KW donor splice site selection; telomere biogenesis; oncogenesis;
 KW apoptosis-associated protein; cancer; tumour formation;
 KW expression inhibition; antisense therapy.
 XX
 OS Homo sapiens.
 XX
 PN US6165789-A.
 XX
 PD 26-DEC-2000.
 XX
 PF 27-OCT-1999; 99US-00428696.
 XX
 PR 27-OCT-1999; 99US-00428696.
 XX
 PA (ISIS-) ISIS PHARM INC.
 XX
 PI Monia BP, Cowsett LM;
 XX
 DR WPI; 2001-090484/10.
 DR N-PSDB; AAC92731.
 XX
 PT Novel antisense compound targeted to human hnRNP A1 which specifically
 PT hybridizes with and inhibits the expression of human hnRNP A1, useful for
 PT modulating the expression of hnRNP A1 in cells.
 XX
 PS Example 16; Col 43-48; 38pp; English.
 XX
 CC This sequence represents human heterogeneous nuclear ribonucleoprotein A1
 CC (hnRNP A1). hnRNP A1 (also known as heterogeneous nuclear
 CC ribonucleoprotein core protein A1 and p40CRS) is thought to function in
 CC the stabilisation, transport and processing (including alternative
 CC splicing) of newly synthesised mRNAs. It facilitates the annealing of
 CC single-stranded nucleic acids, modulates the binding of snRNPs to RNA
 CC intron sequences, and shuttles continuously between the nucleus and the
 CC cytoplasm acting as a carrier protein for mRNAs. hnRNP A1 also
 CC participates in telomere biogenesis, with low levels of hnRNP correlating
 CC with shortened telomeres. In addition, hnRNP A1 has also been classified
 CC as an apoptosis-associated protein on the basis that it is specifically
 CC cleaved into three fragments during antibody-mediated apoptosis. Due to
 CC its ability to control splicing events, particularly donor splice site
 CC selection, hnRNP A1 is implicated in the process of oncogenesis. The
 CC invention relates to antisense oligonucleotides targeted to the hnRNP A1
 CC gene, which inhibit its expression. A series of oligonucleotides
 CC (AAC92738-C92817) were designed to target different regions of the human
 CC hnRNP A1 mRNA, and were analysed for their effect on hnRNP A1 mRNA levels
 CC by quantitative real-time PCR. The oligonucleotides of the invention are
 CC useful for diagnosis, prevention and treatment of conditions associated
 CC with hnRNP A1 expression, such as cancer
 XX
 SQ Sequence 320 AA;
 Query Match 93.8%; Score 228; DB 4; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.7e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSSNFGPMKGNFGRRSSGPGGGGQYFAKPRNQGGYGG 40
 DB 268 NOSSNFGPMKGNFGRRSSGPGGGGQYFAKPRNQGGYGG 307
 RESULT 13
 AAB81934
 ID AAB81934 standard; protein; 320 AA.
 XX
 AC AAB81934;
 XX
 DT 25-JUN-2001 (first entry)
 XX

DE Marmoset vitamin D response element binding protein #1.
 XX
 KW Marmoset; vitamin D response element binding protein; VDRE-BP; lymphoma;
 KW vitamin D resistance; osteoporosis; hypercalcaemia; vitamin D toxicity;
 KW glucocorticoid mediated disorder; granuloma forming disease;
 KW vitamin D intoxication; steroid hormone hypersecretion; gene therapy.
 XX
 OS Saguinus oedipus.
 XX
 PN WO200121649-A2.
 XX
 PD 29-MAR-2001.
 XX
 PF 20-SEP-2000; 2000WO-US025844.
 XX
 PR 22-SEP-1999; 99US-00400967.
 XX
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.
 XX
 PI Adams JS;
 XX
 DR WPI; 2001-308082/32.
 DR N-PSDB; AAP85636.
 XX
 PT New vitamin D response element-binding protein (VDRE-BP) useful in
 PT modifying vitamin D receptor activity, in producing anti-VDRE-BP
 PT antibodies, in identifying agonists and antagonists of the protein, or in
 PT gene therapy.
 XX
 PS Claim 17; Page 71-72; 81pp; English.
 XX
 CC The present invention provides the protein and coding sequences for two
 CC vitamin D response element binding proteins (VDRE-BPs) from the marmoset.
 CC These confer vitamin D resistance on the primate, a characteristic which
 CC is associated with high circulating levels of other steroid hormones. The
 CC sequences provided by the invention can be used to identify treatments
 CC for osteoporosis, hypercalcaemia, vitamin D intoxication, steroid hormone
 CC hypersecretion, glucocorticoid mediated disorders, lymphoma and granuloma
 CC forming diseases. The present sequence is one of the VDRE-BPs of the
 CC invention
 XX
 SQ Sequence 320 AA;
 Query Match 93.8%; Score 228; DB 4; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.7e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSSNFGPMKGNFGRRSSGPGGGGQYFAKPRNQGGYGG 40
 DB 268 NOSSNFGPMKGNFGRRSSGPGGGGQYFAKPRNQGGYGG 307
 RESULT 14
 ABB00955
 ID ABB00955 standard; protein; 320 AA.
 XX
 AC ABB00955;
 XX
 DT 13-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #946.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US008631.
 XX

PR 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 PA (HYSE-) HYSEQ INC.
 XX Drmanac RT, Liu C, Tang YT;
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS65142.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.
 XX
 PS Claim 20; SEQ ID NO 31314; 103pp; English.
 XX
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences. (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have application in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 320 AA;
 Query Match 93.8%; Score 228; DB 4; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.7e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NQSSNFGPMKGNFGGRSGPYGGGQYFAKPRNQGYYG 40
 DB 268 NQSSNFGPMKGNFGGRSGPYGGGQYFAKPRNQGYYG 307
 RESULT 15
 AB357241
 ID ABB57241 standard; protein; 320 AA.
 XX
 AC ABB57241;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:645.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.
 XX
 OS Mus musculus.
 XX
 PN WO200118188-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 18-MAY-2001; 2001WO-JP004192.
 XX
 PR 18-MAY-2000; 2000JP-00145977.
 XX

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 DR WPI; 2002-034733/04.
 DR N-PSDB; ABI99624.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 1623-1625; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 320 AA;
 Query Match 93.8%; Score 228; DB 5; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.7e-18;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NQSSNFGPMKGNFGGRSGPYGGGQYFAKPRNQGYYG 40
 DB 268 NQSSNFGPMKGNFGGRSGPYGGGQYFAKPRNQGYYG 307
 Search completed: October 22, 2004, 13:43:04
 Job time : 161 secs

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OM protein - protein search, using sw model

Run on: October 22, 2004, 13:40:25 ; Search time 37 seconds

(without alignments)

109.219 Million cell updates/sec

Title: US-09-763-982B-1

Perfect score: 243

Sequence: 1 NQSNFGPMKGNFGGRSSG.....GGGGYFAKPRNQGGYGGC 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	228	93.8	320	1 DDRT	helix-destabilizin
2	228	93.8	320	1 A4485	heterogeneous ribo
3	228	93.8	320	2 S04617	heterogeneous ribo
4	228	93.8	320	2 S02061	heterogeneous ribo
5	222	91.4	320	2 S30192	heterogeneous ribo
6	127	52.3	365	2 A34840	heterogeneous ribo
7	123	50.6	346	2 S40775	ribonucleoprotein
8	118	48.6	373	2 S40777	heterogeneous ribo
9	114.5	47.1	385	2 S40778	ribonucleoprotein
10	114	46.9	353	2 B34504	heterogeneous nucl
11	108	44.4	358	2 S40776	ribonucleoprotein
12	107.5	44.2	351	2 B34840	heterogeneous ribo
13	97	39.9	169	1 S38331	glycine-rich RNA-b
14	93.5	38.5	168	1 S12312	glycine-rich RNA-b
15	90	37.0	165	2 T03583	glycine-rich RNA-b
16	89.5	36.8	156	2 S41771	glycine-rich RNA-b
17	87.5	36.0	365	2 A26459	helix-destabilizin
18	87	35.8	173	2 S53050	RNA binding protei
19	85.5	35.2	157	2 S04536	embryonic abundan
20	85	35.0	127	2 S49195	GCR 20 protein - f
21	84.5	34.8	112	2 T22078	hypothetical prote
22	84.5	34.8	220	2 A44805	eggshell protein p
23	84.5	34.8	259	2 T15126	hypothetical prote
24	84.5	34.8	561	2 A31994	keratin 10, type I
25	84	34.6	688	2 T48796	probable ATP-depen
26	83.5	34.4	269	2 I52962	FBRNP - human
27	83.5	34.4	345	1 B41732	heterogeneous nucl
28	83	34.2	166	2 T10463	glycine-rich prote
29	83	34.2	341	2 T27929	hypothetical prote

30	82.5	34.0	169	2 T10465	glycine-rich prote
31	82.5	34.0	334	2 S53490	RNA-binding protei
32	82.5	34.0	604	2 S13653	ATP-dependent RNA
33	82.5	34.0	633	2 H81854	probable ATP-depen
34	82	33.7	161	2 S71453	glycine-rich RNA-b
35	82	33.7	175	2 S54255	probable glycine r
36	81.5	33.5	290	2 T48274	hypothetical prote
37	81.5	33.5	341	2 B75374	conserved hypothet
38	81.5	33.5	593	1 KRHU0	keratin 10, type I
39	81	33.3	145	2 T01356	glycine-rich RNA b
40	81	33.3	386	1 S22315	snRNP-associated p
41	81	33.3	1585	2 T31611	hypothetical prote
42	80.5	33.1	82	2 S19774	glycine-rich prote
43	80.5	33.1	142	2 S12311	glycine-rich RNA-b
44	80.5	33.1	157	1 S14857	glycine-rich prote
45	80	32.9	155	2 S20846	glycine-rich prote

ALIGNMENTS

RESULT 1

DDRT

helix-destabilizing protein - rat

N;Alternate names: single-stranded DNA-binding protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 13-Jun-1997

C;Accession: A02682

R;Cobianchi, F.; SenGupta, D.N.; Zmudzka, B.Z.; Wilson, S.H.

J. Biol. Chem. 261, 3536-3543, 1986

A;Title: Structure of rodent helix-destabilizing protein revealed by cDNA cloning.

A;Reference number: A02682; MUID:86140140; PMID:3005291

A;Accession: A02682

A;Molecule type: mRNA

A;Residues: 1-320 <COB>

C;Comment: This protein was isolated from the brain.

C;Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology

C;Keywords: acetylated amino end; brain; DNA binding; duplication; methylated amino acid

F;13-81/Domain: ribonucleoprotein repeat homology <RNM1>

F;106-172/Domain: ribonucleoprotein repeat homology <RNM2>

F;2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

F;194/Modified site: omega-N,omega-N-dimethylarginine (Arg) #status predicted

Query Match 93.8% Score 228; DB 1; Length 320;

Best Local Similarity 100.0%; Pred. No. 1.6e-17;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 NQSNFGPMKGNFGGRSSGPGYGGGYFAKPRNQGGYGG 40

Db 268 NQSNFGPMKGNFGGRSSGPGYGGGYFAKPRNQGGYGG 307

RESULT 2

A4485

heterogeneous ribonuclear particle protein A1 - mouse

N;Alternate names: helix-destabilizing protein; hnRNP core protein A1; single stranded Dn

C;Species: Mus musculus (house mouse)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: A44485; JC5070; JC5071

R;Ben-David, Y.; Bani, M.R.; Chabot, B.; De Koven, A.; Bernstein, A.

Mol. Cell. Biol. 12, 4449-4455, 1992

A;Title: Retroviral insertions downstream of the heterogeneous nuclear ribonucleoprotein

A;Reference number: A44485; MUID:93024387; PMID:1406633

A;Accession: A44485

A;Molecule type: mRNA

A;Residues: 1-320 <BEN>

A;Cross-references: UNIPROT:P49312; GB:M99167; NID:G193323; PIDN:AAA37633.1; PID:G193324

A;Experimental source: spleen

A;Note: sequence extracted from NCBI backbone (NCBIP:114165)

R;Onishi, Y.; Kizaki, H.

Biochem. Biophys. Res. Commun. 228, 7-13, 1996

A;Title: Molecular cloning of the genes suppressed in RVC lymphoma cells by topoisomerase

A;Reference number: JC5070; MUID:97069646; PMID:8912629

F:15-91/Domain: ribonucleoprotein repeat homology <RRM1>
F:106-172/Domain: ribonucleoprotein repeat homology <RRM2>
C:Species: Xenopus laevis (in mature frog)
F:194/Modified site: acetylated amino end (Ser) #status predicted
F:194/Modified site: omega-N-methylarginine (Arg) #status predicted

Query Match 91.4%; Score 222; DB 2; Length 320;
Best Local Similarity 97.5%; Pred. No. 7e-17; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
|||||
DB 268 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 307
|||||

RESULT 6
A34840
heterogeneous ribonuclear particle protein A1.a - African clawed frog
N/Alternate names: heterogeneous nuclear ribonucleoprotein X1A1
C:Species: Xenopus laevis (African clawed frog)
C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
C:Accession: A34840
R:Kay, B.K.; Sawhney, R.K.; Wilson, S.H.
Proc. Natl. Acad. Sci. U.S.A. 87, 1367-1371, 1990
A:Title: Potential for two isoforms of the A1 ribonucleoprotein in Xenopus laevis.
A:Reference number: A34840; MUID:90160329; PMID:2137612
A:Accession: A34840
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-365 <XAY>
A:Cross-references: UNIPROT:P17130; GB:M31041; NID:G214238; PIDN:AAA49741.1; PID:G214239
C:Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
C:Keywords: alternative splicing; DNA binding; duplication; nucleus
F:15-91/Domain: ribonucleoprotein repeat homology <RRM1>
F:106-172/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 52.3%; Score 127; DB 2; Length 365;
Best Local Similarity 64.3%; Pred. No. 1.4e-06;
Matches 27; Conservative 3; Mismatches 6; Indels 6; Gaps 3;

QY 3 SSNFGPMKGNFGGRSSGPGYGG--GGQYFAKPRNQGGYGGG 41
|||||
DB 324 SSNFGPMKGNFGGRSSGPGYGGG---GSASSSGYGGG 362
|||||

RESULT 7
S40775
ribonucleoprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40775
R:Good, P.J.; Rebbert, M.L.; Dawid, I.B.
Nucleic Acids Res. 21, 999-1006, 1993
A:Title: Three new members of the RNP protein family in Xenopus.
A:Reference number: S40774; MUID:93197168; PMID:8451200
A:Accession: S40775
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-346 <GOO>
A:Cross-references: UNIPROT:P51989; EMBL:L02954; NID:G214740; PIDN:AAA49948.1; PID:G2147
C:Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
F:10-76/Domain: ribonucleoprotein repeat homology <RRM1>
F:101-167/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 50.6%; Score 123; DB 2; Length 346;
Best Local Similarity 64.4%; Pred. No. 3.7e-06;
Matches 29; Conservative 1; Mismatches 9; Indels 6; Gaps 3;

QY 2 QSSNFGPMK--GNFGGRSS---GPGYGG--GQYFAKPRNQGGYGG 40
|||||
DB 298 QSSNFGPMKSGGNFGGRSSGPGYGGGNGPQNASGNGGGYGG 342
|||||

RESULT 8

S40777
heterogeneous ribonuclear particle protein A3 - African clawed frog
N/Alternate names: heterogeneous nuclear ribonucleoprotein A3
C:Species: Xenopus laevis (African clawed frog)
C:Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C:Accession: S40777; S41738
R:Good, P.J.; Rebbert, M.L.; Dawid, I.B.
Nucleic Acids Res. 21, 999-1006, 1993
A:Title: Three new members of the RNP protein family in Xenopus.
A:Reference number: S40774; MUID:93197168; PMID:8451200
A:Accession: S40777
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-373 <GOO1>
A:Cross-references: UNIPROT:P51968; EMBL:L02956
R:Good, P.J.; Lai, M.; Rebbert, M.L.; Dawid, I.B.
submitted to the EMBL Data Library, October 1992
A:Reference number: S41738
A:Accession: S41738
A:Molecule type: mRNA
A:Residues: 1-85 'S', 87-346, 'S', 348-373 <GOO2>
A:Cross-references: EMBL:L02956; NID:G214744; PIDN:AAA49949.1; PID:G214745
C:Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
F:28-94/Domain: ribonucleoprotein repeat homology <RRM1>
F:119-185/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 48.6%; Score 118; DB 2; Length 373;
Best Local Similarity 55.6%; Pred. No. 1.4e-05;
Matches 25; Conservative 2; Mismatches 6; Indels 12; Gaps 2;

QY 2 QSSNFGPMKGNF-----GGRSSGPGYGGGQYFAKPRNQGGYGGG 41
|||||
DB 327 QSSNFGPMKGSFGRSSGGRGSGPYGGG-----YGSGGGGGGG 364
|||||

RESULT 9
S40778
ribonucleoprotein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40778
R:Good, P.J.; Rebbert, M.L.; Dawid, I.B.
Nucleic Acids Res. 21, 999-1006, 1993
A:Title: Three new members of the RNP protein family in Xenopus.
A:Reference number: S40774; MUID:93197168; PMID:8451200
A:Accession: S40778
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-385 <GOO>
A:Cross-references: UNIPROT:P51992; EMBL:L02957; NID:G214746; PIDN:AAA49950.1; PID:G21474
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1992
C:Superfamily: helix-destabilizing protein; ribonucleoprotein repeat homology
F:28-94/Domain: ribonucleoprotein repeat homology <RRM1>
F:119-185/Domain: ribonucleoprotein repeat homology <RRM2>

Query Match 47.1%; Score 114.5; DB 2; Length 385;
Best Local Similarity 52.1%; Pred. No. 3.4e-05;
Matches 25; Conservative 2; Mismatches 10; Indels 11; Gaps 2;

QY 2 QSSNFGPMKGNF-----GGRSSGPGYGGGQYFAKPRNQGGYGGG 41
|||||
DB 334 QSSNFGPMKAGNFGRSTGTGGSGSSGPGYGGG---YGSGGGGGGGGG 378
|||||

RESULT 10
B34504
heterogeneous nuclear ribonucleoprotein B1 - human
N/Alternate names: heterogeneous ribonuclear particle protein B1; hnRNP protein B1; NEPHC
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 09-Jul-2004
C:Accession: A56845; B34504; A34504; S48057; PC222; B61013; B56845
R:Kozu, T.; Henrich, B.; Schaefer, K.P.

Best Local Similarity 51.4%; Pred. No. 0.0012; Matches 18; Conservative 2; Mismatches 15; Indels 0; Gaps 0;

QY 7 GPMKGNFGGRSSGPGYGGGGYFAKPRNQGGYGGG 41
DB 91 GORGGGYGRGGGGYGGGGYGRGGGGYGGG 125

RESULT 14

S12312
glycine-rich RNA-binding protein (clone S2) - sorghum
C:Species: Sorghum bicolor (sorghum)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S12312
R:Cretin, C.; Puigdomenech, P.
Plant Mol. Biol. 15, 783-785, 1990
A:Title: Glycine-rich RNA-binding proteins from Sorghum vulgare.
A:Reference number: S12311; MUID:91346715; PMID:1715211
A:Accession: S12312
A:Molecule type: mRNA
A:Residues: 1-168 <CR>
A:Cross-references: UNIPROT:Q99070; EMBL:X57662; NID:g21624; PIDN:CAA40862.1; PID:g21625
A:Note: In the authors' translation two additional Gly are shown after 110-Gly
C:Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
C:Keywords: GTP binding
F:9-76/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 38.5%; Score 93.5; DB 1; Length 168;
Best Local Similarity 56.2%; Pred. No. 0.0028;
Matches 18; Conservative 2; Mismatches 11; Indels 1; Gaps 1;

QY 11 GGNFGRRSSGPY-GGGGGYFAKPRNQGGYGGG 41
DB 100 GGGYGRGGYGGGGYGGGGYGRGGGGYGGG 131

RESULT 15

T03583
glycine-rich RNA-binding protein - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03583
R:Lee, M.C.; Kim, C.S.; Yi, B.Y.; Lee, J.S.; Eun, M.Y.
submitted to the EMBL Data Library, June 1997
A:Description: Isolation and characterization of RNA-binding glycine rich protein of rice
A:Reference number: Z14958
A:Accession: T03583
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-165 <LEE>
A:Cross-references: UNIPROT:O24184; EMBL:AF009411; NID:g2267592; PIDN:AAB63589.1; PID:g2
A:Experimental source: cv. Milyang 23
C:Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
F:9-76/Domain: ribonucleoprotein repeat homology <RRM>

Query Match 37.0%; Score 90; DB 2; Length 165;
Best Local Similarity 58.1%; Pred. No. 0.0066;
Matches 18; Conservative 2; Mismatches 9; Indels 2; Gaps 1;

QY 11 GGNFGRRSSGPYGGGGYFAKPRNQGGYGGG 41
DB 103 GGGYGRGGYGGGGYGGGGY-GQRRGGYGGG 131

Search completed: October 22, 2004, 13:47:49
Job time : 38 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 22, 2004, 13:37:19 ; Search time 194 Seconds
(without alignments)
124.566 Million cell updates/sec

Title: US-09-763-982B-1

Perfect score: 243

Sequence: 1 NQSNFGPMKGNFGGRSSG.....GGGGQYFAKPRNQGGYGGC 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 02.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	228	93.8	298	2 Q9BSM5	Q9BSM5 homo sapien
2	228	93.8	313	2 Q6P6G9	Q6P6G9 rattus norv
3	228	93.8	313	2 AAH62235	AAH62235 rattus norv
4	228	93.8	319	1 ROA1_MOUSE	P49312 mus musculus
5	228	93.8	319	1 ROA1_RAT	P04256 rattus norv
6	228	93.8	320	2 Q6IPF2	Q6IPF2 homo sapien
7	228	93.8	320	2 AAH12158	AAH12158 homo sapi
8	228	93.8	320	2 AAH33714	AAH33714 homo sapi
9	228	93.8	320	2 AAH02355	AAH02355 homo sapi
10	228	93.8	320	2 AAH09600	AAH09600 homo sapi
11	228	93.8	320	2 AAH70315	AAH70315 homo sapi
12	228	93.8	320	2 AAH71945	AAH71945 homo sapi
13	228	93.8	371	1 ROA1_HUMAN	P09651 homo sapien
14	222	91.4	319	1 ROA1_MACMU	Q28521 macaca mula
15	219	90.1	70	2 Q9H4S1	Q9H4S1 homo sapien
16	127	52.3	365	1 ROA1_XENLA	P17130 xenopus lae
17	127	52.3	365	2 Q6I229	Q6I229 xenopus lae
18	127	52.3	365	2 AAH2090	AAH2090 xenopus lae
19	125	51.4	63	2 Q8NFG3	Q8NFG3 homo sapien
20	125	51.4	193	2 Q70592	Q70592 rattus norv
21	125	51.4	318	2 Q6P6I7	Q6P6I7 mus musculus
22	125	51.4	318	2 AAH62198	AAH62198 mus muscu
23	125	51.4	357	2 AAQ63631	AAQ63631 rattus norv
24	125	51.4	378	1 ROA3_HUMAN	P51991 homo sapien
25	125	51.4	378	1 AAQ63629	AAQ63629 homo sapi
26	125	51.4	379	1 ROA3_MOUSE	Q8B905 mus musculus
27	125	51.4	379	1 ROA3_RAT	Q6URK4 rattus norv
28	125	51.4	379	2 AAQ63630	AAQ63630 rattus norv
29	125	51.4	379	2 AAH64824	AAH64824 mus muscu
30	123	50.6	346	1 RO21_XENLA	P51989 xenopus lae
31	120	49.4	388	2 Q7SXQ3	Q7SXQ3 brachydanio

Q6nyw8 brachydanio
AAH66434 brachydan
Q7zwv4 xenopus lae
P51968 xenopus lae
P51992 xenopus lae
Q6PCV9 mus musculu
AAH59107 mus muscu
Q8C280 mus musculu
Q8B569 mus musculu
Q9TTV2 saguinus oe
Q912z9 mus musculu
P22626 homo sapien
Q8CJ71 mus musculu
Q803K3 brachydanio

ALIGNMENTS

RESULT 1

Q9BSM5 ID Q9BSM5 PRELIMINARY; PRT; 298 AA.
AC Q9BSM5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004945; AAH04945.1; -
DR InterAct; Q9BSM5; -
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; RRM_1; 2.
DR SMART; SM00360; RRM; 2.
DR PROSITE; PS50102; RRM; 2.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 298 AA; 31752 MW; 8A4CDFCB838D78BB CRC64;

Query Match 93.8%; Score 228; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.1e-16;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 40
DB 246 NQSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGGYGG 285

RESULT 2

Q6P6G9 ID Q6P6G9 PRELIMINARY; PRT; 313 AA.
AC Q6P6G9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hnrp1 protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary gland;
 RA Strausberg R.;
 RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC062235; AAH62235.1; - - - - -
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; RRM_1; 2.
 DR SMART: SM00360; RRM; 2.
 DR PROSITE: PS0102; RRM; 2.
 DR PROSITE: PS0030; RRM_RNP_1; UNKNOWN 2.
 SQ SEQUENCE 313 AA; 33620 MW; AE0EEC10972DEF7D CRC64;

Query Match 93.8%; Score 228; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPGMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 |||||
 DB 261 NQSNFPGMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 300
 |||||

RESULT 3
 AAH62235 PRELIMINARY; PRT; 313 AA.
 ID AAH62235
 AC AAH62235
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hirpal protein.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary gland;
 RA Strausberg R.;
 RA Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC062235; AAH62235.1; - - - - -
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; RRM_1; 2.
 DR SMART: SM00360; RRM; 2.
 DR PROSITE: PS0102; RRM; 2.
 DR PROSITE: PS0030; RRM_RNP_1; UNKNOWN 2.
 SQ SEQUENCE 313 AA; 33620 MW; AE0EEC10972DEF7D CRC64;

Query Match 93.8%; Score 228; DB 2; Length 313;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPGMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 |||||
 DB 261 NQSNFPGMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 300
 |||||

RESULT 4
 ROAL MOUSE
 ID ROAL MOUSE STANDARD; PRT; 319 AA.
 AC P49312; P97312;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing
 DE protein) (Single-strand binding protein) (hnRNP core protein A1) (HDP-
 DE 1) (Topoisomerase-inhibitor suppressed).
 GN Name=HnRpa1; Synonyms=Fli-2, Tis;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93024387; PubMed=1406633;
 RA Ben-David Y., Bani M.R., Chabot B., de Koven A., Bernstein A.;
 RT "Retroviral insertions downstream of the heterogeneous nuclear
 RT ribonucleoprotein A1 gene in erythroleukemia cells: evidence that A1
 RT is not essential for cell growth.";
 RL Mol. Cell. Biol. 12:4449-4455 (1992).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoma;
 RX MEDLINE=97069646; PubMed=8912629;
 RA Onishi Y., Kizaki H.;
 RT "Molecular cloning of the genes suppressed in RVC lymphoma cells by
 RT topoisomerase inhibitors.";
 RL Biochem. Biophys. Res. Commun. 228:7-13 (1996).
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Thymus;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaide I., Osato N., Saito R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldairelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.B., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Naglot D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido I., Favan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,

FT DOMAIN 13 96 RNA-binding (RRM) 1.
 FT DOMAIN 104 183 RNA-binding (RRM) 2.
 FT DOMAIN 217 239 RNA-binding RGG-box.
 FT DOMAIN 194 319 Gly-rich.
 FT DOMAIN 267 304 NUCLEAR TARGETING SEQUENCE (BY SIMILARITY).
 FT DOMAIN 307 312 Poly-Ser.
 FT MOD_RES 5 5 Phosphoserine (By similarity).
 FT MOD_RES 193 193 Asymmetric dimethylarginine.
 FT MOD_RES 312 312 Phosphoserine (By similarity).
 FT CONFLICT 8 E -> G (in Ref. 3).
 SQ SEQUENCE 319 AA; 34081 MW; CSBEYD183456B303 CRC64;

Query Match 93.8%; Score 228; DB 1; Length 319;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 DB 267 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 306

RESULT 6

Q61PF2 PRELIMINARY; PRT; 320 AA.
 AC Q61PF2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein A1, isoform a.
 GN Name=NRPA1; (Human).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RP "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC071945; AAH71945.1; -;
 DR InterPro; IPR000504; RNA_rec_mot.
 DR Pfam; PF00076; RRM_1; 2.
 DR SMART; SM00360; RRM; 2.
 DR PROSITE; PS0102; RRM; 2.
 DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_2.
 KW Nucleocapsid; Ribonucleoprotein.
 SQ SEQUENCE 320 AA; 34180 MW; 9069C6B408DE1AF3 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 DB 268 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 307

RESULT 7

AAH12158 PRELIMINARY; PRT; 320 AA.
 AC AAH12158;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein A1, isoform a.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RP "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC012158; AAH12158.1; -;
 KW Nucleocapsid; Ribonucleoprotein.
 SQ SEQUENCE 320 AA; 34196 MW; 59485C9FA1FF8A1 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 DB 268 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 307

RESULT 8

AAH33714 PRELIMINARY; PRT; 320 AA.
 AC AAH33714;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein A1, isoform a.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primata; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

TISSUE=Lymph;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Frazer K.A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Kettman M., Madan A., Rodriguez A.C., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Touchman J.W., Green E.D., Dickinson M.C., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

[2]

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Lymph;

Strausberg R.;

Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

EMBL; BC033714; AAH33714.1; -.

Nucleocapsid; Ribonucleoprotein.

SEQUENCE 320 AA; 34196 MW; 59485C9FA1FF8AE1 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;

Best Local Similarity 100.0%; Pred. No. 2.2e-16;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 40

DB 268 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 307

AAHQ2355 PRELIMINARY; PRT; 320 AA.

ID AAHQ2355

AC AAHQ2355;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Heterogeneous nuclear ribonucleoprotein A1, isoform a.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

TISSUE=Lung;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Frazer K.A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Kettman M., Madan A., Rodriguez A.C., Touchman J.W., Green E.D., Dickinson M.C., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

[2]

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Lymph;

Strausberg R.;

Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

EMBL; BC033714; AAH33714.1; -.

Nucleocapsid; Ribonucleoprotein.

SEQUENCE 320 AA; 34196 MW; 59485C9FA1FF8AE1 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;

Best Local Similarity 100.0%; Pred. No. 2.2e-16;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 40

DB 268 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 307

AAHQ2355 PRELIMINARY; PRT; 320 AA.

ID AAHQ2355

AC AAHQ2355;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Heterogeneous nuclear ribonucleoprotein A1, isoform a.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

TISSUE=Lung;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Frazer K.A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Kettman M., Madan A., Rodriguez A.C., Touchman J.W., Green E.D., Dickinson M.C., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

[2]

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Lymph;

Strausberg R.;

Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

EMBL; BC033714; AAH33714.1; -.

Nucleocapsid; Ribonucleoprotein.

SEQUENCE 320 AA; 34196 MW; 59485C9FA1FF8AE1 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;

Best Local Similarity 100.0%; Pred. No. 2.2e-16;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 40

DB 268 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 307

AAHQ2355 PRELIMINARY; PRT; 320 AA.

ID AAHQ2355

AC AAHQ2355;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DE 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Heterogeneous nuclear ribonucleoprotein A1, isoform a.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

TISSUE=Lung;

MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Frazer K.A., Young A.C., Shevchenko Y., Bouffard G.G., Whiting M., Madan A., Kettman M., Madan A., Rodriguez A.C., Touchman J.W., Green E.D., Dickinson M.C., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

[2]

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

SEQUENCE FROM N.A.

TISSUE=Lymph;

Strausberg R.;

Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

EMBL; BC033714; AAH33714.1; -.

Nucleocapsid; Ribonucleoprotein.

SEQUENCE 320 AA; 34196 MW; 59485C9FA1FF8AE1 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;

Best Local Similarity 100.0%; Pred. No. 2.2e-16;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 40

DB 268 NQSNFPMKMGNGFNFGSSGPGYGGGQYFAKPRNQGGYGG 307

AAHQ2355 PRELIMINARY; PRT; 320 AA.

ID AAHQ2355

AC AAHQ2355;

DT 02-MAR-2004 (TrEMBLrel

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 DB 268 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 307

RESULT 11

AAH70315 PRELIMINARY; PRT; 320 AA.
 AC AAH70315;
 DT 13-MAY-2004 (TREMELrel. 27, Created)
 DT 13-MAY-2004 (TREMELrel. 27, Last sequence update)
 DE HNRPA1 protein.
 GN HNRPA1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC070315; AAH70315.1; - 59485C9FAPF8AE1 CRC64;
 SQ SEQUENCE 320 AA; 34196 MW; 59485C9FAPF8AE1 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 DB 268 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 307

RESULT 12

AAH71945 PRELIMINARY; PRT; 320 AA.
 AC AAH71945;
 DT 01-JUN-2004 (TREMELrel. 27, Created)
 DT 01-JUN-2004 (TREMELrel. 27, Last sequence update)
 DE Heterogeneous nuclear ribonucleoprotein A1 (Helix-stabilizing
 GN HNRPA1.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;

RN SEQUENCE FROM N.A.
 RP TISSUE=Skin;
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC071945; AAH71945.1; -
 RL Nucleocapsid: Ribonucleoprotein.
 SQ SEQUENCE 320 AA; 34180 MW; 9069C6B408DE1AF3 CRC64;

Query Match 93.8%; Score 228; DB 2; Length 320;
 Best Local Similarity 100.0%; Pred. No. 2.2e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 40
 DB 268 NOSSNFGPMKGNFGGRSSGPGYGGGQYFAKPRNQGYYG 307

RESULT 13

ROA1_HUMAN STANDARD; PRT; 371 AA.
 ID ROA1_HUMAN STANDARD; PRT; 371 AA.
 AC P09651.

DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-OCT-2004 (Rel. 45, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein A1 (Helix-stabilizing
 DE protein) (Single-strand binding protein) (hnRNP core protein A1).
 GN Name=HNRPA1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A. (ISOFORM A1-A).
 RC TISSUE=Liver;
 RX MEDLINE=89342435; PubMed=2760922;

RA Biamonti G., Buvoili M., Bassi M.T., Morandi C., Cobiainchi F., Riva S.;
 RT "Isolation of an active gene encoding human hnRNP protein A1. Evidence
 RT for alternative splicing";
 RL J. Mol. Biol. 207:491-503(1989).
 RN [2]

RP SEQUENCE FROM N.A. (ISOFORM A1-A).
 RC TISSUE=Fibroblast;
 RX MEDLINE=88233978; PubMed=2836799;

RA Buvoili M., Biamonti G., Ghetti A., Riva S., Bassi M.T., Morandi C.;
 RT "cDNA cloning of human hnRNP protein A1 reveals the existence of
 RT multiple mRNA isoforms";
 RL Nucleic Acids Res. 16:3751-3770(1988).
 RN [3]

FT TURN 73 73
 FT STRAND 77 78
 FT TURN 79 80
 FT STRAND 81 82
 FT STRAND 84 87
 FT STRAND 105 112
 FT TURN 113 114
 FT HELIX 117 124
 FT TURN 125 127
 FT STRAND 130 137
 FT TURN 139 141
 FT STRAND 144 152
 FT HELIX 155 162
 FT TURN 163 163
 FT STRAND 168 169
 FT TURN 170 171
 FT STRAND 172 173
 FT STRAND 175 178
 SQ SEQUENCE 371 AA; 38715 MW; B3EEFA5AE1DB7C26 CRC64;
 Query Match 93.8%; Score 228; DB 1; Length 371;
 Best Local Similarity 100.0%; Pred. No. 2.5e-16;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 NOSSNFGPMKGNFGRRSSGPGYGGGQYFAKPRNQGYYGG 40
 DB 319 NOSSNFGPMKGNFGRRSSGPGYGGGQYFAKPRNQGYYGG 358
 RESULT 14
 ID ROAL MACMU STANDARD; PRT; 319 AA.
 AC Q28521;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heterogeneous nuclear ribonucleoprotein A1 (Helix-destabilizing
 DE protein) (Single-strand binding protein) (hnRNP core protein A1).
 GN Name=HNRPA1;
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 GN NCB1_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tracheobronchial epithelium;
 RX MEDLINE=93192320; PubMed=8448206;
 RA An G., Wu R.;
 RT "CDNA cloning of a hnRNP A1 isoform and its regulation by retinol in
 RT monkey tracheobronchial epithelial cells.";
 RL Biochim. Biophys. Acta 1172:292-300(1993)
 CC -|- FUNCTION: Involved in the packaging of pre-mRNA into hnRNP
 CC particles, transport of poly(A) mRNA from the nucleus to the
 CC cytoplasm and may modulate splice site selection.
 CC -|- SUBCELLULAR LOCATION: Nuclear. Shuttles continuously between the
 CC nucleus and the cytoplasm along with mRNA. Component of
 CC ribonucleosomes.
 CC -|- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL; M84334; AAB01436.1; -;
 CC FIR; S30192; S30192.
 CC HSSP; P09651; 2UPI.
 CC InterPro; IPR000504; RNA_rec_mot.
 CC Pfam; PF00076; RRM_1; 2.

DR PROSITE; PS50102; RRM; 2.
 DR PROSITE; PS00030; RRM_RNP_1; 2.
 KW Methylation; mRNA transport; Nuclear protein; Phosphorylation; Repeat;
 KW Ribonucleoprotein; RNA-binding; Transport.
 FT INIT MET 0 0
 FT DOMAIN 3 93
 FT DOMAIN 94 184
 FT DOMAIN 13 96
 FT DOMAIN 104 183
 FT DOMAIN 217 239
 FT DOMAIN 194 319
 FT DOMAIN 267 304
 FT MOD_RES 5 5
 FT MOD_RES 193 193
 FT MOD_RES 312 312
 FT MOD_RES 307 312
 FT POLY-SER.
 SQ SEQUENCE 319 AA; 34089 MW; 5A04D9E3BFD969E3 CRC64;
 Query Match 91.4%; Score 222; DB 1; Length 319;
 Best Local Similarity 97.5%; Pred. No. 9.6e-16;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NOSSNFGPMKGNFGRRSSGPGYGGGQYFAKPRNQGYYGG 40
 DB 267 NOSSNFGPMKGNFGRRSSGPGYGGGQYFAKPRNQGYYGG 306
 RESULT 15
 ID Q9H4S1 PRELIMINARY; PRT; 70 AA.
 AC Q9H4S1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE BA438F9.2 (Novel protein similar to heterogeneous nuclear
 DE ribonucleoprotein A1 (HNRPA1)) (Fragment).
 GN Name=BA438F9.2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bates K.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL390738; CAC12722.1; -;
 DR GO; GO:0030529; C:ribonucleoprotein complex; IEA.
 DR GO; GO:0019013; C:viral nucleocapsid; IEA.
 KW Nucleocapsid; Ribonucleoprotein.
 FT NON_TER 1
 SQ SEQUENCE 70 AA; 7084 MW; 44379598BA26329E CRC64;
 Query Match 90.1%; Score 219; DB 2; Length 70;
 Best Local Similarity 97.5%; Pred. No. 4.7e-16;
 Matches 39; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 NOSSNFGPMKGNFGRRSSGPGYGGGQYFAKPRNQGYYGG 40
 DB 18 NOSSNFGPMKGNFGRRSSGPGYGGGQYFAKPRNQGYYGG 57

Search completed: October 22, 2004, 13:46:24
 Job time : 197 secs